

## SEQUENCE LISTING

<110> Lovejoy, David  
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 Rotzinger, Susan

<120> TENEURIN C-TERMINAL ASSOCIATED PEPTIDES (TCAP) AND METHODS AND USES THEREOF

<130> 090931-360630

<140> US 10/510,959

<141> 2005-08-10

<150> PCT/CA03/00622

<151> 2003-05-02

<150> US 60/376,879

<151> 2002-05-02

<150> US 60/377,231

<151> 2002-05-03

<150> US 60/424,016

<151> 2002-11-06

<160> 138

<170> PatentIn version 3.1

<210> 1

<211> 1490

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout Ten M3 carboxy termini'

<400> 1

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gtggtcacca acgctctgaa catcgccaac gaggactgca tcaaggctgc cgccgtcctc	240
aacaatgcgt tctacctgga ggacctgcac ttcacgggtgg agggacgcga cacgcactac	300
ttcatcaaga ccagcctccc ggagagcgac ctgggagcgc tgaggctgac aagcgggagg	360
aagtcgctgg agaacggaag tcaacgtgac tgtgtcccag tccaccaccg tgggtgaacgg	420
cagaaccggc gcttcgcoga cgtggagctg cagtacggcg ctctagcgt ccacgtgcgc	480

tatggcatga ctctggacga ggagaaggcg cgtgtgctgg agcaggccag gcagaaggcg	540
ttgtcgagtg cctgggtccag ggagcaacaa cgggtgaggg agggggagga gggggtgagg	600
ctgtggacgg agggggagaa gaggcagctg ctgagcggga ggaaggttct gggctacgac	660
gggtactacg tcctctccat agagcagtac cccgagctag cagactccgc taacaacatc	720
cagttcctca ggcagagcga aatagggaag aggtaacaga cagaatcctc ggcactggcc	780
gccaaagaga ctacccctc caaatcctgc ccccaacct ccctcgctc ccccttttc	840
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agtaaaatgt agaatatctt aaactgaact atacctaata ctaccactgt ggggcctgaa	960
aatcaaaciaa acgggtcca actgacgcaa atgtttgtcc catgtgctat acagcgttga	1020
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tcctgacgac tgaccttga ttgaccttg cgtactgaaa aaggtagtgt tgttgctcgc	1320
agtaggacca tgggtctcca atgggtgtaa ctagacagtt aaaaccactt gttgaaacca	1380
cttgcttggt cttctgcttt tctttccaaa agggacaaaa cagctccac caagtgactt	1440
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&lt;210&gt; 2

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rainbow Trout Ten M3 coding sequence of carboxy termini of Ten M3

&lt;400&gt; 2

tccatctcgg gggtgcaaca ggaagtgacc cggcaagcca aggctttcct gtccttcgag	60
aggatgccgg agatccagct gagccgccgg cgctccaacc gggagaaacc ctggctgtgg	120
ttcgccaccg ccaagtctct gatcggttaag ggtgtcatgt tggcgggtgac gcagggccgt	180
gtggtcacca acgctctgaa catcgccaac gaggactgca tcaaggctcg cgccgtcctc	240
aacaatgcgt tctacctgga ggacctgcac ttcacggtgg agggacgcga cacgcactac	300
ttcatcaaga ccagcctccc ggagagcgac ctgggagcgc tgaggctgac aagcgggagg	360

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aagtcgctgg agaacggaag tcaacgtgac tgtgtcccag tccaccaccg tggatgaacgg 420
cagaaccggc gcttcgccga cgtggagctg cagtacggcg ctctagcgct ccacgtgcgc 480
tatggcatga ctctggacga ggagaaggcg cgtgtgctgg agcaggccag gcagaaggcg 540
ttgtcgagtg cctgggtccag ggagcaacaa cgggtgaggg agggggagga gggggtgagg 600
ctgtggacgg agggggagaa gaggcagctg ctgagcggga ggaaggttct gggctacgac 660
gggtactacg tcctctccat agagcagtag cccgagctag cagactccgc taacaacatc 720
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<210> 3
<211> 251
<212> PRT
<213> Artificial Sequence

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<220>
<223> Rainbow Trout Ten M3 carboxy termini of Ten M3

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<400> 3

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```

Ser Ile Ser Gly Val Gln Gln Glu Val Thr Arg Gln Ala Lys Ala Phe
1           5           10          15

```

```

Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser
          20           25           30

```

```

Asn Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Ala Lys Ser Leu Ile
          35           40           45

```

```

Gly Lys Gly Val Met Leu Ala Val Thr Gln Gly Arg Val Val Thr Asn
50           55           60

```

```

Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
65           70           75           80

```

```

Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly Arg
          85           90           95

```

```

Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu Gly
          100          105          110

```

```

Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val Asn
          115          120          125

```

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg  
 130 135 140

Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val Arg  
 145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln Ala  
 165 170 175

Arg Gln Lys Ala Leu Ser Ser Ala Trp Ser Arg Glu Gln Gln Arg Val  
 180 185 190

Arg Glu Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys Arg  
 195 200 205

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val  
 210 215 220

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
 225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
 245 250

<210> 4  
 <211> 252  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mouse Ten M1

<400> 4

Met Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe  
 1 5 10 15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Gln Tyr Asn Glu Gly Arg  
 20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val  
 35 40 45

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Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Glu Gly Ile Val Thr Ala  
50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile  
65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly  
85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu  
100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val  
115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg  
130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile  
145 150 155 160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Met  
165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Gln Glu Gln Arg Arg  
180 185 190

Leu Gln Glu Gly Glu Glu Gly Thr Arg Val Trp Thr Glu Gly Glu Lys  
195 200 205

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
210 215 220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
245 250

<210> 5

<211> 253

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse Ten M2

&lt;400&gt; 5

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe  
 1 5 10 15

Leu Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile  
 20 25 30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly  
 35 40 45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val  
 50 55 60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn  
 65 70 75 80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp  
 85 90 95

Thr His Tyr Phe Val Lys Ile Gly Ala Ala Asp Gly Asp Leu Val Thr  
 100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val  
 115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe  
 130 135 140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr  
 145 150 155 160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp  
 165 170 175

Gln Ala Gly Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln  
 180 185 190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu  
 195 200 205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr  
 210 215 220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser  
 225 230 235 240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg  
 245 250

<210> 6  
 <211> 251  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mouse Ten M3

<400> 6

Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe  
 1 5 10 15

Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Lys Ala  
 20 25 30

Gly Ala Glu Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile  
 35 40 45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn  
 50 55 60

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu  
 65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys  
 85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly  
 100 105 110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn  
 115 120 125

8/77

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg  
130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg  
145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala  
165 170 175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val  
180 185 190

Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg  
195 200 205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val  
210 215 220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
245 250

<210> 7  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mouse Ten M4

<400> 7

Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe  
1 5 10 15

Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser  
20 25 30

Cys Gln Gln Ala Pro Glu Thr Lys Lys Phe Ala Ser Ser Gly Ser Ile  
35 40 45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr  
50 55 60



9/77

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Ile Ala Ala Ile  
65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly  
85 90 95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu  
100 105 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val  
115 120 125

Asn Val Thr Val Ser Gln Ile Asn Thr Met Leu Ile Gln Leu Gln Tyr  
130 135 140

Arg Ala Leu Cys Leu Asn Thr Arg Tyr Gly Thr Thr Val Asp Glu Glu  
145 150 155 160

Lys Val Arg Val Leu Glu Leu Ala Arg Gln Arg Ala Val Arg Gln Ala  
165 170 175

Trp Ala Arg Glu Gln Gln Arg Leu Arg Glu Gly Glu Glu Gly Leu Arg  
180 185 190

Ala Trp Thr Asp Gly Glu Lys Gln Gln Val Leu Asn Thr Gly Arg Val  
195 200 205

Gln Gly Tyr Asp Gly Phe Phe Val Thr Ser Val Glu Gln Tyr Pro Glu  
210 215 220

Leu Ser Asp Ser Ala Asn Asn Ile His Phe Met Arg Gln Ser Glu Met  
225 230 235 240

Gly Arg Arg

<210> 8  
<211> 252  
<212> PRT  
<213> Artificial Sequence

<220>

10/77

<223> Human Ten M1

<400> 8

Thr Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe  
1 5 10 15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Arg Tyr Asn Asp Gly Arg  
20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val  
35 40 45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala  
50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile  
65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly  
85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu  
100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val  
115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg  
130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile  
145 150 155 160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Ile  
165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Lys Glu Gln Arg Arg  
180 185 190

Leu Gln Glu Gly Glu Glu Gly Ile Arg Ala Trp Thr Glu Gly Glu Lys  
195 200 205

11/77

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
210 215 220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
245 250

<210> 9  
<211> 253  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human Ten M2

<400> 9

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe  
1 5 10 15

Met Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile  
20 25 30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly  
35 40 45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val  
50 55 60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn  
65 70 75 80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp  
85 90 95

Thr His Tyr Phe Val Lys Ile Gly Ser Ala Asp Gly Asp Leu Val Thr  
100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val  
115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe  
130 135 140

12/77

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr  
145 150 155 160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp  
165 170 175

Gln Ala Arg Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln  
180 185 190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu  
195 200 205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr  
210 215 220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser  
225 230 235 240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg  
245 250

<210> 10  
<211> 251  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human Ten M3

<400> 10

Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe  
1 5 10 15

Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Arg Ala  
20 25 30

Gly Gly Ala Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile  
35 40 45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn  
50 55 60

13/77

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu  
65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys  
85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly  
100 105 110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn  
115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg  
130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg  
145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala  
165 170 175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val  
180 185 190

Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg  
195 200 205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val  
210 215 220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg  
245 250

<210> 11  
<211> 252  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human Ten M4

14/77

<400> 11

Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe  
1 5 10 15

Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser  
20 25 30

Cys Leu Gln Ala Pro Lys Thr Lys Lys Phe Ala Ser Ser Gly Ser Val  
35 40 45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr  
50 55 60

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Val Ala Ala Ile  
65 70 75 80

Leu Asn His Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly  
85 90 95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu  
100 105 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val  
115 120 125

Asn Val Thr Val Ser Gln Ile Asn Thr Val Leu Ser Gly Arg Thr Arg  
130 135 140

Arg Tyr Thr Asp Ile Gln Leu Gln Tyr Gly Ala Leu Cys Leu Asn Thr  
145 150 155 160

Arg Tyr Gly Thr Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Leu  
165 170 175

Ala Arg Gln Arg Ala Val Arg Gln Ala Trp Ala Arg Glu Gln Gln Arg  
180 185 190

Leu Arg Glu Gly Glu Glu Gly Leu Arg Ala Trp Thr Glu Gly Glu Lys  
195 200 205

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe  
210 215 220

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn  
 225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg  
 245 250

<210> 12  
 <211> 252  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish Ten M3

<400> 12

Ser Ile Ser Gly Val Gln Gln Glu Val Met Arg Gln Ala Lys Ala Phe  
 1 5 10 15

Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser  
 20 25 30

Ser Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile  
 35 40 45

Gly Lys Gly Val Met Leu Ala Ile Thr Ser Lys Gly Gln Val Ala Thr  
 50 55 60

Asn Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Val Thr Val  
 65 70 75 80

Leu Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly  
 85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu  
 100 105 110

Gly Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val  
 115 120 125

Asn Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg  
 130 135 140

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Arg Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val  
145 150 155 160

Arg Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln  
165 170 175

Ala Arg Gln Arg Ala Leu Ser Ser Ala Trp Ala Arg Glu Gln Gln Arg  
180 185 190

Val Arg Asp Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys  
195 200 205

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr  
210 215 220

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
225 230 235 240

Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
245 250

<210> 13  
<211> 40  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Rainbow Trout TCAP3 (40a.a.)

<400> 13

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val  
1 5 10 15

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile  
35 40

<210> 14  
<211> 41  
<212> PRT  
<213> Artificial Sequence

<220>



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<223> Rainbow Trout TCAP 3 (41a.a.)

<400> 14

Arg Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile  
35 40

<210> 15

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (43 a.a.)

<400> 15

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val  
1 5 10 15

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
35 40

<210> 16

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (44 a.a.)

<400> 16

Arg Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
 35 40

<210> 17  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Rainbow Trout TCAP3 (120 n.a.)

<400> 17  
 cagctgctga gcgggaggaa ggttctgggc tacgacgggt actacgtcct ctccatagag 60  
 cagtaccccg agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata 120

<210> 18  
 <211> 123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Rainbow Trout TCAP3 (123 n.a.)

<400> 18  
 aggcagctgc tgagcgggag gaaggttctg ggctacgacg ggtactacgt cctctccata 60  
 gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa 120  
 ata 123

<210> 19  
 <211> 129  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Rainbow Trout preTCAP3 (129 n.a.)

<400> 19  
 cagctgctga gcgggaggaa ggttctgggc tacgacgggt actacgtcct ctccatagag 60  
 cagtaccccg agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata 120  
 gggaagagg 129

<210> 20  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence

<220>

19/77

<223> Rainbow Trout preTCAP3 (132 n.a.)

<400> 20  
aggcagctgc tgagcgggag gaaggttctg ggctacgacg ggtactacgt cctctccata 60  
gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa 120  
ataggaaga gg 132

<210> 21

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP3 (40 a.a.)

<400> 21

Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val  
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile  
35 40

<210> 22

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP3 (41 a.a.)

<400> 22

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

Val Gln Phe Leu Arg Gln Ser Glu Ile  
35 40

<210> 23

<211> 43

20/77

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Zebrafish preTCAP3 (43 a.a.)

<400> 23

Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val  
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
35 40

<210> 24  
<211> 44  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Zebrafish preTCAP3 (44 a.a.)

<400> 24

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
35 40

<210> 25  
<211> 120  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Zebrafish TCAP3 (120 n.a.)

<400> 25  
cagttgctca gctctgggaa ggtgctgggt tacgatgggt actatgtact atcagtggag 60  
caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgaata 120

<210> 26  
 <211> 123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish TCAP3 (123 n.a.)

<400> 26  
 aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg 60  
 gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag 120  
 ata 123

<210> 27  
 <211> 129  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish TCAP3 (129 n.a.)

<400> 27  
 cagttgctca gctctgggaa ggtgctgggt tacgatgggt actatgtact atcagtggag 60  
 caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgaata 120  
 gggaagagg 129

<210> 28  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish preTCAP3 (132 n.a.)

<400> 28  
 aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg 60  
 gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag 120  
 ataggaaga gg 132

<210> 29  
 <211> 40  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish TCAP4 (40 a.a.)

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<400> 29

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile  
1 5 10 15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val  
20 25 30

His Phe Trp Arg Gln Thr Glu Met  
35 40

<210> 30

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP4 (41 a.a.)

<400> 30

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr  
1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn  
20 25 30

Val His Phe Trp Arg Gln Thr Glu Met  
35 40

<210> 31

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP4 (43 a.a.)

<400> 31

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile  
1 5 10 15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val  
20 25 30

His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg  
35 40

<210> 32  
 <211> 44  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish preTCAP4 (44 a.a.)

<400> 32

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr  
 1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn  
 20 25 30

Val His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg  
 35 40

<210> 33  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish TCAP4 (120 n.a.)

<400> 33  
 cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac 60  
 cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg 120

<210> 34  
 <211> 123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish TCAP4 (123 n.a.)

<400> 34  
 cagcagctcc taagctctgg acgtgtacag ggctacgaag gcttctacat agtatcagtc 60  
 gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag 120  
 atg 123

<210> 35  
 <211> 129

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish preTCAP4 (129 n.a.)

<400> 35  
 cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac 60  
 cagttccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg 120  
 ggacgcagg 129

<210> 36  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish preTCAP4 (132 n.a.)

<400> 36  
 cagcagctcc taagctctgg acgtgtacag ggctacgaag gcttctacat agtatcagtc 60  
 gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag 120  
 atgggacgca gg 132

<210> 37  
 <211> 40  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mouse TCAP1 (40 a.a.)

<400> 37  
 Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val  
 1 5 10 15  
 Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile  
 20 25 30  
 His Phe Met Arg Gln Ser Glu Ile  
 35 40

<210> 38  
 <211> 41  
 <212> PRT  
 <213> Artificial Sequence



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<220>

<223> Mouse TCAP1 (41 a.a.)

<400> 38

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile  
35 40

<210> 39

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP1 (43 a.a.)

<400> 39

Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile  
20 25 30

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
35 40

<210> 40

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP1 (44 a.a.)

<400> 40

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
 35 40

<210> 41  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mouse TCAP1 (120 n.a.)

<400> 41  
 cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag 60  
 cagtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaata 120

<210> 42  
 <211> 123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mouse TCAP1 (123 n.a.)

<400> 42  
 cagcagcttt tgggcaccgg gaggggtgcag gggatatgatg ggtattttgt cttgtctgtt 60  
 gagcagtatt tagaactttc agacagtgcc aacaatatcc acttcatgag acagagtgaa 120  
 ata 123

<210> 43  
 <211> 129  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mouse preTCAP1 (129 n.a.)

<400> 43  
 cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag 60  
 cagtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaata 120  
 ggcaggagg 129

<210> 44  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP1 (132 n.a.)

&lt;400&gt; 44

cagcagcttt tgggcacccg gaggggtgcag gggatatgatg ggtattttgt cttgtctgtt 60

gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa 120

ataggcagga gg 132

&lt;210&gt; 45

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP2 (40 a.a.)

&lt;400&gt; 45

Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr	Val
1				5				10					15		

Leu	Pro	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn	Ile
		20					25					30			

Gln	Phe	Leu	Arg	Gln	Asn	Glu	Ile
	35				40		

&lt;210&gt; 46

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP2 (41 a.a.)

&lt;400&gt; 46

Gln	Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Pro	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn
		20						25					30		

Ile	Gln	Phe	Leu	Arg	Gln	Asn	Glu	Met
	35					40		

<210> 47  
 <211> 43  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mouse preTCAP2 (43 a.a)

<400> 47

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val  
 1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile  
 20 25 30

Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg  
 35 40

<210> 48  
 <211> 44  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mouse preTCAP2 (44 a.a.)

<400> 48

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr  
 1 5 10 15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn  
 20 25 30

Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg  
 35 40

<210> 49  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mouse TCAP2 (120 n.a.)

<400> 49  
 caactcctga gcacgggacg ggtacaaggt tatgagggtt attacgtact tccgggtggaa 60  
 cagtacccgg agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagagg 120

<210> 50  
 <211> 123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mouse TCAP 2 (123 n.a.)

<400> 50  
 cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg 60  
 gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag 120  
 atg 123

<210> 51  
 <211> 129  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mouse preTCAP2 (129 n.a.)

<400> 51  
 caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa 60  
 cagtaccgag agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagatg 120  
 ggaaagagg 129

<210> 52  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mouse preTCAP2 (132 n.a.)

<400> 52  
 cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg 60  
 gaacagtacc cggagctggc agacagtagc agcaacatcc agttotthaag acagaatgag 120  
 atgggaaaga gg 132

<210> 53  
 <211> 40  
 <212> PRT  
 <213> Artificial Sequence

<220>

30/77

<223> Mouse TCAP3 (40 a.a.)

<400> 53

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile  
35 40

<210> 54

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP3 (41 a..a)

<400> 54

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile  
35 40

<210> 55

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP3 (43 a.a.)

<400> 55

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
20 25 30

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Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
35 40

<210> 56  
<211> 44  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mouse preTCAP3 (44 a.a.)

<400> 56

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
35 40

<210> 57  
<211> 120  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mouse TCAP3 (120 n.a.)

<400> 57  
cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag 60  
cagtaccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc 120

<210> 58  
<211> 123  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mouse TCAP3 (123 n.a.)

<400> 58  
cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcgggtg 60  
gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag 120  
atc 123

<210> 59  
 <211> 129  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mouse preTCAP3 (129 n.a.)

<400> 59  
 cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag 60  
 cagtaccccg agctggctga cagtccaac aacatccagt tcttgcgaca aagtgagatc 120  
 ggcaagagg 129

<210> 60  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mouse preTCAP3 (132 n.a.)

<400> 60  
 cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcgggtg 60  
 gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag 120  
 atcggcaaga gg 132

<210> 61  
 <211> 40  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mouse TCAP4 (40 a.a.)

<400> 61  
 Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val  
 1 5 10 15  
 Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile  
 20 25 30  
 His Phe Met Arg Gln Ser Glu Met  
 35 40

<210> 62  
 <211> 41



<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mouse TCAP4 (41 a.a.)

<400> 62

Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe  
 1 5 10 15

Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn  
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Met  
 35 40

<210> 63  
 <211> 43  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mouse preTCAP4 (43 a.a.)

<400> 63

Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val  
 1 5 10 15

Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile  
 20 25 30

His Phe Met Arg Gln Ser Glu Met Gly Arg Arg  
 35 40

<210> 64  
 <211> 44  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mouse preTCAP4 (44 a.a.)

<400> 64

Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe  
 1 5 10 15

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Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn  
20 25 30

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg  
35 40

<210> 65  
<211> 120  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mouse TCAP4 (120 n.a.)

<400> 65  
caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag 60  
cagtaccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg 120

<210> 66  
<211> 123  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mouse TCAP4 (123 n.a.)

<400> 66  
cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc 60  
gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag 120  
atg 123

<210> 67  
<211> 129  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mouse preTCAP4 (129 n.a.)

<400> 67  
caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag 60  
cagtaccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg 120  
ggccgaagg 129

<210> 68  
<211> 132

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP4 (132 n.a.)

&lt;400&gt; 68

cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc 60

gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag 120

atgggccgaa gg 132

&lt;210&gt; 69

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP1 (40 a.a.)

&lt;400&gt; 69

Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Phe	Val
1				5				10						15	

Leu	Ser	Val	Glu	Gln	Tyr	Leu	Glu	Leu	Ser	Asp	Ser	Ala	Asn	Asn	Ile
			20					25					30		

His	Phe	Met	Arg	Gln	Ser	Glu	Ile
				35			40

&lt;210&gt; 70

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP1 (41 a.a.)

&lt;400&gt; 70

Gln	Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Phe
1				5					10					15	

Val	Leu	Ser	Val	Glu	Gln	Tyr	Leu	Glu	Leu	Ser	Asp	Ser	Ala	Asn	Asn
				20				25						30	

Ile	His	Phe	Met	Arg	Gln	Ser	Glu	Ile
					35			40

<210> 71  
 <211> 43  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP1 (43 a.a.)

<400> 71

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val  
 1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile  
 20 25 30

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
 35 40

<210> 72  
 <211> 44  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP1 (44 a.a.)

<400> 72

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
 1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
 35 40

<210> 73  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human TCAP1 (120 n.a.)

<400> 73  
 cagcttttga gcactgggcg ggtacaagggt tacgatgggt attttgtttt gtctgttgag 60

cagtatttag aactttctga cagtgccaat aatattcact ttatgagaca gagcgaaata 120

<210> 74  
 <211> 123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human TCAP1 (123 n.a.)

<400> 74  
 cagcagcttt tgagcactgg gcgggtacaa ggttacgatg ggtattttgt tttgtctggt 60  
 gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa 120  
 ata 123

<210> 75  
 <211> 129  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP1 (129 n.a.)

<400> 75  
 cagcttttga gcactgggcg ggtacaaggt tacgatgggt attttgttt gtctgttgag 60  
 cagtatttag aactttctga cagtgccaat aatattcact ttatgagaca gagcgaaata 120  
 ggcaggagg 129

<210> 76  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP1 (132 n.a.)

<400> 76  
 cagcagcttt tgagcactgg gcgggtacaa ggttacgatg ggtattttgt tttgtctggt 60  
 gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa 120  
 ataggcagga gg 132

<210> 77  
 <211> 40  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP2 (40 a.a.)

&lt;400&gt; 77

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val  
 1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile  
 20 25 30

Gln Phe Leu Arg Gln Asn Glu Met  
 35 40

&lt;210&gt; 78

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP2 (41 a.a.)

&lt;400&gt; 78

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr  
 1 5 10 15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn  
 20 25 30

Ile Gln Phe Leu Arg Gln Asn Glu Met  
 35 40

&lt;210&gt; 79

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP2 (43 a.a.)

&lt;400&gt; 79

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val  
 1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile  
 20 25 30

Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg  
           35                          40

<210> 80  
 <211> 44  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP2 (44 a.a.)

<400> 80

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr  
 1                          5                          10                          15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn  
                           20                          25                          30

Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg  
           35                          40

<210> 81  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human TCAP2 (120 n.a.)

<400> 81  
 cagcttctga gcaccgggcg cgtgcaaggg tacgagggat attacgtgct tcccgtggag 60  
 caatacccag agcttgca ga tagcagc aacatccagt ttttaagaca gaatgagatg 120

<210> 82  
 <211> 123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human TCAP2 (123 n.a.)

<400> 82  
 cagcagcttc tgagcaccgg gcgcgtgcaa gggtacgagg gatattacgt gcttcccgtg 60  
 gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag 120  
 atg 123

<210> 83  
 <211> 129  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP2 (129 n.a.)

<400> 83  
 cagcttctga gcaccgggcg cgtgcaaggg tacgagggat attacgtgct tcccgtggag 60  
 caatacccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg 120  
 ggaaagagg 129

<210> 84  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP2 (132 n.a.)

<400> 84  
 cagcagcttc tgagcaccgg gcgcgtgcaa gggtagcagg gatattacgt gcttcccgtg 60  
 gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag 120  
 atgggaaaga gg 132

<210> 85  
 <211> 40  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human TCAP3 (40 a.a.)

<400> 85

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val  
 1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
 20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile  
 35 40



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<210> 86  
<211> 41  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human TCAP3 (41 a.a.)

<400> 86

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile  
35 40

<210> 87  
<211> 43  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human preTCAP3 (43 a.a.)

<400> 87

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg  
35 40

<210> 88  
<211> 44  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human preTCAP3 (44 a.a.)

<400> 88

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
                   20                  25                  30

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg  
           35                  40

<210> 89  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human TCAP3 (120 n.a.)

<400> 89  
 cagctgctga gcgccggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag 60  
 cagtaccccc agctggccga cagcgccaac aacatccagt tcctgcggca gagcgagatc 120

<210> 90  
 <211> 123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human TCAP3 (123 n.a.)

<400> 90  
 cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcggtg 60  
 gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag 120  
 atc 123

<210> 91  
 <211> 129  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP (129 n.a.)

<400> 91  
 cagctgctga gcgccggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag 60  
 cagtaccccc agctggccga cagcgccaac aacatccagt tcctgcggca gagcgagatc 120  
 ggaggagg 129

<210> 92  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP3 (132 n.a.)

<400> 92  
 cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcggcg 60  
 gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag 120  
 atcggcagga gg 132

<210> 93  
 <211> 40  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human TCAP4 (40 a.a.)

<400> 93  
 Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val  
 1 5 10 15  
 Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile  
 20 25 30  
 His Phe Met Arg Gln Ser Glu Met  
 35 40

<210> 94  
 <211> 41  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human TCAP4 (41 a.a.)

<400> 94  
 Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe  
 1 5 10 15  
 Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn  
 20 25 30

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Ile His Phe Met Arg Gln Ser Glu Met  
35 40

<210> 95  
<211> 43  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human preTCAP4 (43 a..a)

<400> 95

Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val  
1 5 10 15

Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile  
20 25 30

His Phe Met Arg Gln Ser Glu Met Gly Arg Arg  
35 40

<210> 96  
<211> 44  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human preTCAP4 (44 a.a.)

<400> 96

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe  
1 5 10 15

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn  
20 25 30

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg  
35 40

<210> 97  
<211> 120  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Human TCAP4 (120 n.a.)

<400> 97  
 caggtgctga gcacagggcg ggtgcaaggc tacgacggct ttttcgtgat ctctgtcgag 60  
 cagtaccag aactgtcaga cagcgccaac aacatccact tcatgagaca gagcgagatg 120

<210> 98  
 <211> 123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human TCAP4 (123 n.a.)

<400> 98  
 cagcaggtgc tgagcacagg gcgggtgcaa ggctacgacg gctttttcgt gatctctgtc 60  
 gagcagtacc cagaactgtc agacagcgcc aacaacatcc acttcatgag acagagcgag 120  
 atg 123

<210> 99  
 <211> 129  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP4 (129 n.a.)

<400> 99  
 caggtgctga gcacagggcg ggtgcaaggc tacgacggct ttttcgtgat ctctgtcgag 60  
 cagtaccag aactgtcaga cagcgccaac aacatccact tcatgagaca gagcgagatg 120  
 ggccggagg 129

<210> 100  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human preTCAP4 (132 n.a.)

<400> 100  
 cagcaggtgc tgagcacagg gcgggtgcaa ggctacgacg gctttttcgt gatctctgtc 60  
 gagcagtacc cagaactgtc agacagcgcc aacaacatcc acttcatgag acagagcgag 120  
 atgggccgga gg 132

<210> 101  
 <211> 41

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> G. gallus TCAP-1

<400> 101

Gln Gln Leu Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
 1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile  
 35 40

<210> 102  
 <211> 41  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Zebrafish TCAP-4

<400> 102

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr  
 1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn  
 20 25 30

Val His Phe Trp Arg Gln Thr Glu Met  
 35 40

<210> 103  
 <211> 37  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> D. melanogaster Ten-m gene product

<400> 103

Glu Leu Val Gln His Gly Asp Val Asp Gly Trp Asn Gly Asp Ile His  
 1 5 10 15

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Ser Ile His Lys Tyr Pro Gln Leu Ala Asp Pro Gly Asn Val Ala Phe  
20 25 30

Gln Arg Asp Ala Lys  
35

<210> 104

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Human CRF TCAP like region

<400> 104

Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg  
1 5 10 15

Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His  
20 25 30

Ser Asn Arg Lys Leu Met Glu Ile Ile  
35 40

<210> 105

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Human urocortin TCAP-like region

<400> 105

Asp Asn Pro Ser Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr  
1 5 10 15

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln  
20 25 30

Asn Arg Ile Ile Phe Asp Ser Val  
35 40

<210> 106

<211> 38

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human urocortin 2 TCAP-like region

&lt;400&gt; 106

Ile Val Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Gln Ile Leu Leu  
 1 5 10 15

Glu Gln Ala Arg Ala Arg Ala Ala Arg Glu Gln Ala Thr Thr Asn Ala  
 20 25 30

Arg Ile Leu Ala Arg Val  
 35

&lt;210&gt; 107

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human urocortin 3 TCAP-like region

&lt;400&gt; 107

Phe Thr Leu Ser Leu Asp Val Pro Thr Asn Ile Met Asn Leu Leu Phe  
 1 5 10 15

Asn Ile Ala Lys Ala Lys Asn Leu Arg Ala Gln Ala Ala Ala Asn Ala  
 20 25 30

His Leu Met Ala Gln Ile  
 35

&lt;210&gt; 108

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; L. migratoria DP

&lt;400&gt; 108

Met Gly Met Gly Pro Ser Leu Ser Ile Val Asn Pro Met Asp Val Leu  
 1 5 10 15

Arg Gln Arg Leu Leu Leu Glu Ile Ala Arg Arg Arg Leu Arg Asp Ala  
 20 25 30



Glu Glu Gln Ile Lys Ala Asn Lys Asp Phe Leu Gln Gln Ile  
           35                          40                          45

<210> 109  
 <211> 46  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A. domesticus DP

<400> 109

Thr Gly Ala Gln Ser Leu Ser Ile Val Ala Pro Leu Asp Val Leu Arg  
 1                          5                          10                          15

Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Arg Met Arg Glu Leu Gln  
                           20                          25                          30

Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile  
           35                          40                          45

<210> 110  
 <211> 39  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> T. molitor DP

<400> 110

Ser Pro Thr Ile Ser Ile Thr Ala Pro Ile Asp Val Leu Arg Lys Thr  
 1                          5                          10                          15

Trp Glu Gln Glu Arg Ala Arg Lys Gln Met Val Ala Gln Asn Asn Arg  
                           20                          25                          30

Glu Phe Leu Asn Ser Leu Asn  
           35

<210> 111  
 <211> 41  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> M. sexta DP-1

<400> 111

Arg	Met	Pro	Ser	Leu	Ser	Ile	Asp	Leu	Pro	Met	Ser	Val	Leu	Arg	Gln
1				5				10					15		

Lys	Leu	Ser	Leu	Glu	Lys	Glu	Arg	Lys	Val	His	Ala	Leu	Arg	Ala	Ala
			20				25						30		

Ala	Asn	Arg	Asn	Phe	Leu	Asn	Asp	Ile
	35					40		

<210> 112

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> M. sexta DP-II

<400> 112

Ser	Leu	Ser	Val	Asn	Pro	Ala	Val	Asp	Ile	Leu	Gln	His	Arg	Tyr	Met
1				5				10					15		

Glu	Lys	Val	Ala	Gln	Asn	Asn	Arg	Asn	Phe	Leu	Asn	Arg	Val
			20				25					30	

<210> 113

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> P. Americana

<400> 113

Thr	Gly	Ser	Gly	Pro	Ser	Leu	Ser	Ile	Val	Asn	Pro	Leu	Asp	Val	Leu
1				5				10					15		

Arg	Gln	Arg	Leu	Leu	Leu	Glu	Ile	Ala	Arg	Arg	Arg	Met	Arg	Gln	Ser
			20				25						30		

Gln	Asp	Gln	Ile	Gln	Asn	Arg	Glu	Ile	Leu	Gln	Thr	Ile
			35				40					45

51/77

<210> 114  
<211> 41  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> O. keta CRP

<400> 114

Ser Asp Asp Pro Pro Ile Ser Leu Asp Leu Thr Phe His Met Leu Arg  
1 5 10 15

Gln Met Asn Glu Met Ser Arg Ala Glu Gln Leu Gln Gln Gln Ala His  
20 25 30

Ser Asn Arg Lys Met Met Glu Ile Phe  
35 40

<210> 115  
<211> 40  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> R. norvegicus

<400> 115

Asp Asp Pro Pro Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr  
1 5 10 15

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln  
20 25 30

Asn Arg Ile Ile Phe Asp Ser Val  
35 40

<210> 116  
<211> 37  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> P. sauvageii

<400> 116

Gln Gly Pro Pro Ile Ser Ile Asp Leu Ser Leu Glu Leu Leu Arg Lys  
1 5 10 15

Met Ile Glu Ile Glu Lys Gln Glu Lys Glu Lys Gln Gln Ala Ala Asn  
                   20                  25                  30

Asn Arg Leu Leu Leu  
                   35

<210> 117  
 <211> 41  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> C. carpio US

<400> 117

Asn Asp Asp Pro Pro Ile Ser Ile Asp Leu Thr Phe His Leu Leu Arg  
 1                  5                  10                  15

Asn Met Ile Glu Met Ala Arg Asn Glu Asn Gln Arg Glu Gln Ala Gly  
                   20                  25                  30

Leu Asn Arg Lys Tyr Leu Asp Glu Val  
                   35                  40

<210> 118  
 <211> 38  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> M. Musculus UCN2

<400> 118

Val Ile Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Arg Ile Leu Leu  
 1                  5                  10                  15

Glu Gln Ala Arg Tyr Lys Ala Ala Arg Asn Gln Ala Ala Thr Asn Ala  
                   20                  25                  30

Gln Ile Leu Ala His Val  
                   35

<210> 119  
 <211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> R. dano UCN2

<400> 119

Leu Thr Leu Ser Leu Asp Val Pro Thr Asn Ile Met Asn Val Leu Phe  
1 5 10 15

Asp Val Ala Lys Ala Lys Asn Leu Arg Ala Lys Ala Ala Glu Asn Ala  
20 25 30

Arg Leu Leu Ala His Ile  
35

<210> 120

<211> 305

<212> DNA

<213> Artificial Sequence

<220>

<223> Hamster 305bp urocortin cDNA probe examples "cloning mRNA"

<400> 120

attcacgcc gctcgggatc tgagcctgca ggcgagcggc agcgacggga agaccttccg 60  
ctgtccatcg acctcacatt ccacctgcta cggaccctgc tggagatggc ccggacacag 120  
agccaacgcy agcgagcaga gcagaaccga atcataactca acgcgggtggg caagtgatcg 180  
gcccgggtgtg ggacccccaaa aggctcgacc ctttccccta cctaccccgg ggctgaagtc 240  
acgcgaccga agtcggctta gtcccgcggg gcagcgcctc ccagagttac cctgaacaat 300  
cccg 305

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> TCAP1 fwd primer

<400> 121

acgtcagtgt tgatgggagg acta 24

<210> 122

<211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TCAP1 rvs primer

<400> 122  
 cctcctgcct atttcactct gtctcat

27

<210> 123  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TCAP2 Fwd primer

<400> 123  
 tcgagggcaa ggacacacac tactt

25

<210> 124  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TCAP2 rvs primer

<400> 124  
 aagaactgga tggtgctgct actgtc

26

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TCAP3 fwd primer

<400> 125  
 caacaacgcc ttctacctgg agaac

25

<210> 126  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TCAP3 rvs primer

<400> 126

tgttggtggc actgtcagcc a

21

<210> 127  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TCAP4 fwd primer

<400> 127  
 ttgcctcca gtggttccat ctt

23

<210> 128  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TCAP4 rvs primer

<400> 128  
 tggatattgt tggcgctgac tgac

24

<210> 129  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Conserved motif between CRF and TCAP I/L S X X (X)-L/V at amino terminus

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(1)  
 <223> X=I or L

<220>  
 <221> MISC\_FEATURE  
 <222> (3)..(3)  
 <223> X=T or A

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X=L, I or G

<220>  
 <221> MISC\_FEATURE  
 <222> (5)..(5)  
 <223> X=D, R or K

<220>  
 <221> MISC\_FEATURE  
 <222> (6)..(6)  
 <223> X=L or V

<400> 129

Xaa Ser Xaa Xaa Xaa Xaa  
 1 5

<210> 130  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Conserved motif between CRF and TCAP - In middle L/V-L/I-X-V/aliphatic residue

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(1)  
 <223> X=V or L

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(2)  
 <223> X=L, I or F

<220>  
 <221> MISC\_FEATURE  
 <222> (3)..(3)  
 <223> X=E, N, S or P

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X=M, L Q, I or V

<400> 130

Xaa Xaa Xaa Xaa  
 1

<210> 131  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Conserved motif between CRF and TCAP N/I/A-H/basic residue -I/L/F/-aliphatic at carboxy terminus

<220>  
 <221> MISC\_FEATURE



<222> (2)..(2)  
 <223> X=R, A or I

<220>  
 <221> MISC\_FEATURE  
 <222> (3)..(3)  
 <223> X=H or basic residues, K, I, R or Q

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X=I, L or F

<400> 131

Asn Xaa Xaa Xaa  
 1

<210> 132  
 <211> 8964  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> exon  
 <222> (50)..(8197)

<400> 132  
 aagttctaag aagccggacc gatgtgcaca gagaaggaat gaaggaagt atg gat gtg 58  
 Met Asp Val  
 1

aag gaa cgc agg cct tac tgc tcc ttg acc aag agc aga cgg gaa aag 106  
 Lys Glu Arg Arg Pro Tyr Cys Ser Leu Thr Lys Ser Arg Arg Glu Lys  
 5 10 15

gaa agg cgc tat aca aat tcg tcc gcg gac aat gag gag tgt agg gtc 154  
 Glu Arg Arg Tyr Thr Asn Ser Ser Ala Asp Asn Glu Glu Cys Arg Val  
 20 25 30 35

ccc acg cag aag tcc tat agt tcc agt gaa acc ttg aaa gct ttc gat 202  
 Pro Thr Gln Lys Ser Tyr Ser Ser Ser Glu Thr Leu Lys Ala Phe Asp  
 40 45 50

cat gat tat tca cgg ctg ctt tat gga aac aga gta aag gat ttg gtc 250  
 His Asp Tyr Ser Arg Leu Leu Tyr Gly Asn Arg Val Lys Asp Leu Val  
 55 60 65

cac aga gaa gcc gac gag tat act aga caa gga cag aat ttt acc cta 298  
 His Arg Glu Ala Asp Glu Tyr Thr Arg Gln Gly Gln Asn Phe Thr Leu  
 70 75 80

agg cag tta gga gtg tgt gaa tcc gca act cga aga gga gtg gca ttc 346  
 Arg Gln Leu Gly Val Cys Glu Ser Ala Thr Arg Arg Gly Val Ala Phe

85	90	95	
tgt gcg gaa atg ggg ctc cct cac aga ggt tac tcc atc agt gca ggg Cys Ala Glu Met Gly Leu Pro His Arg Gly Tyr Ser Ile Ser Ala Gly 100 105 110 115			394
tca gat gcg gat acg gaa aac gaa gca gtg atg tcc cct gag cat gcc Ser Asp Ala Asp Thr Glu Asn Glu Ala Val Met Ser Pro Glu His Ala 120 125 130			442
atg aga ctt tgg ggc agg ggg gtc aaa tcg ggc cgc agt tcc tgc ctg Met Arg Leu Trp Gly Arg Gly Val Lys Ser Gly Arg Ser Ser Cys Leu 135 140 145			490
tca agc cgg tcc aac tcc gcc ctc acc ctg aca gac acg gag cac gag Ser Ser Arg Ser Asn Ser Ala Leu Thr Leu Thr Asp Thr Glu His Glu 150 155 160			538
aac agg tcg gac agt gag agc gag caa cct tca aac aac cca ggg caa Asn Arg Ser Asp Ser Glu Ser Glu Gln Pro Ser Asn Asn Pro Gly Gln 165 170 175			586
ccc acc ctg cag cct ttg ccg cca tcc cac aag cag cac ccg gcg cag Pro Thr Leu Gln Pro Leu Pro Pro Ser His Lys Gln His Pro Ala Gln 180 185 190 195			634
cat cac ccg tcc atc act tcc ctc aat aga aac tcc ctg acc aat aga His His Pro Ser Ile Thr Ser Leu Asn Arg Asn Ser Leu Thr Asn Arg 200 205 210			682
agg aac cag agt ccg gcc ccg ccg gct gct ttg ccc gcc gag ctg caa Arg Asn Gln Ser Pro Ala Pro Pro Ala Ala Leu Pro Ala Glu Leu Gln 215 220 225			730
acc aca ccc gag tcc gtc cag ctg cag gac agc tgg gtc ctt ggc agt Thr Thr Pro Glu Ser Val Gln Leu Gln Asp Ser Trp Val Leu Gly Ser 230 235 240			778
aat gta cca ctg gaa agc agg cat ttc cta ttc aaa aca ggg aca ggg Asn Val Pro Leu Glu Ser Arg His Phe Leu Phe Lys Thr Gly Thr Gly 245 250 255			826
acg acg cca ctg ttc agt acg gca acc ccg gga tac aca atg gca tct Thr Thr Pro Leu Phe Ser Thr Ala Thr Pro Gly Tyr Thr Met Ala Ser 260 265 270 275			874
ggc tct gtt tat tct ccg cct acc cgg cca ctt cct aga aac acc cta Gly Ser Val Tyr Ser Pro Pro Thr Arg Pro Leu Pro Arg Asn Thr Leu 280 285 290			922
tca aga agt gct ttt aaa ttc aag aag tct tca aag tac tgc agc tgg Ser Arg Ser Ala Phe Lys Phe Lys Lys Ser Ser Lys Tyr Cys Ser Trp 295 300 305			970
agg tgc acc gca ctg tgt gct gta ggg gtc tca gtg ctc ctg gcc att Arg Cys Thr Ala Leu Cys Ala Val Gly Val Ser Val Leu Leu Ala Ile			1018

310	315	320	
ctc ctc tcc tat ttt ata gca atg cat cta ttt ggc ctc aac tgg cac Leu Leu Ser Tyr Phe Ile Ala Met His Leu Phe Gly Leu Asn Trp His 325 330 335			1066
tta cag cag acg gaa aat gac aca ttc gag aat gga aaa gtg aat tct Leu Gln Gln Thr Glu Asn Asp Thr Phe Glu Asn Gly Lys Val Asn Ser 340 345 350 355			1114
gac acc gtg cca aca aac act gta tcg tta cct tct ggc gac aat gga Asp Thr Val Pro Thr Asn Thr Val Ser Leu Pro Ser Gly Asp Asn Gly 360 365 370			1162
aaa tta ggt gga ttt aca cat gaa aat aac acc ata gat tcc gga gaa Lys Leu Gly Gly Phe Thr His Glu Asn Asn Thr Ile Asp Ser Gly Glu 375 380 385			1210
ctt gat att ggc cgg aga gca att caa gag gtt ccc ccc ggg atc ttc Leu Asp Ile Gly Arg Arg Ala Ile Gln Glu Val Pro Pro Gly Ile Phe 390 395 400			1258
tgg aga tcg cag ctc ttt att gat cag cca cag ttt ctt aag ttc aac Trp Arg Ser Gln Leu Phe Ile Asp Gln Pro Gln Phe Leu Lys Phe Asn 405 410 415			1306
atc tct ctt cag aag gat gca ttg atc gga gtg tac ggc cgg aag ggc Ile Ser Leu Gln Lys Asp Ala Leu Ile Gly Val Tyr Gly Arg Lys Gly 420 425 430 435			1354
tta ccg cct tcc cat act cag tac gac ttt gtg gaa cta ctg gat ggt Leu Pro Pro Ser His Thr Gln Tyr Asp Phe Val Glu Leu Leu Asp Gly 440 445 450			1402
agc agg tta att gcg aga gag cag cgg aac ctg gtg gag tcc gaa aga Ser Arg Leu Ile Ala Arg Glu Gln Arg Asn Leu Val Glu Ser Glu Arg 455 460 465			1450
gcc ggg cgg cag gcg aga tct gtc agc ctg cac gaa gct ggc ttc atc Ala Gly Arg Gln Ala Arg Ser Val Ser Leu His Glu Ala Gly Phe Ile 470 475 480			1498
cag tac ttg gat tct gga atc tgg cat ctg gct ttt tat aac gac ggg Gln Tyr Leu Asp Ser Gly Ile Trp His Leu Ala Phe Tyr Asn Asp Gly 485 490 495			1546
aaa aac cca gag cag gtc tcc ttt aac acg atc gtt ata gag tct gtg Lys Asn Pro Glu Gln Val Ser Phe Asn Thr Ile Val Ile Glu Ser Val 500 505 510 515			1594
gtg gaa tgc ccc cga aat tgc cat gga aat gga gag tgt gtt tct gga Val Glu Cys Pro Arg Asn Cys His Gly Asn Gly Glu Cys Val Ser Gly 520 525 530			1642
act tgc cat tgt ttc ccc ggg ttt cta ggt ccg gat tgt tca aga gca Thr Cys His Cys Phe Pro Gly Phe Leu Gly Pro Asp Cys Ser Arg Ala			1690

535	540	545	
gcc tgt ccg gtg ctc tgt agt ggc aac ggg caa tac tcc aag ggc cgc Ala Cys Pro Val Leu Cys Ser Gly Asn Gly Gln Tyr Ser Lys Gly Arg 550 555 560			1738
tgc ctg tgc ttc agt ggc tgg aag ggc acc gag tgt gac gtg ccg acg Cys Leu Cys Phe Ser Gly Trp Lys Gly Thr Glu Cys Asp Val Pro Thr 565 570 575			1786
acc cag tgc att gac ccg cag tgc ggg ggt cgt ggg att tgc atc atg Thr Gln Cys Ile Asp Pro Gln Cys Gly Gly Arg Gly Ile Cys Ile Met 580 585 590 595			1834
ggc tct tgc gct tgt aac tcg gga tac aaa gga gaa aac tgt gag gaa Gly Ser Cys Ala Cys Asn Ser Gly Tyr Lys Gly Glu Asn Cys Glu Glu 600 605 610			1882
gcg gac tgt cta gac cct gga tgt tct aat cac ggg gtg tgt atc cat Ala Asp Cys Leu Asp Pro Gly Cys Ser Asn His Gly Val Cys Ile His 615 620 625			1930
ggg gaa tgt cac tgc aat cca ggc tgg ggt ggc agc aac tgt gaa ata Gly Glu Cys His Cys Asn Pro Gly Trp Gly Gly Ser Asn Cys Glu Ile 630 635 640			1978
ctg aag act atg tgt gca gac cag tgc tca ggc cac ggg act tac ctt Leu Lys Thr Met Cys Ala Asp Gln Cys Ser Gly His Gly Thr Tyr Leu 645 650 655			2026
caa gaa agc ggc tcc tgc act tgc gac cca aat tgg act ggc ccc gac Gln Glu Ser Gly Ser Cys Thr Cys Asp Pro Asn Trp Thr Gly Pro Asp 660 665 670 675			2074
tgc tca aat gaa ata tgt tca gtg gac tgc ggc tca cac ggc gtc tgc Cys Ser Asn Glu Ile Cys Ser Val Asp Cys Gly Ser His Gly Val Cys 680 685 690			2122
atg ggg ggc tcc tgt cgc tgt gaa gaa ggc tgg acc ggc ccg gcg tgt Met Gly Gly Ser Cys Arg Cys Glu Glu Gly Trp Thr Gly Pro Ala Cys 695 700 705			2170
aat cag aga gct tgc cac cct cgc tgt gct gag cac ggg acg tgc aag Asn Gln Arg Ala Cys His Pro Arg Cys Ala Glu His Gly Thr Cys Lys 710 715 720			2218
gac ggc aag tgc gag tgc agc caa gga tgg aac gga gag cac tgc aca Asp Gly Lys Cys Glu Cys Ser Gln Gly Trp Asn Gly Glu His Cys Thr 725 730 735			2266
att gct cac tat ttg gat aag ata gtt aaa gag ggt tgc ccc ggc ttg Ile Ala His Tyr Leu Asp Lys Ile Val Lys Glu Gly Cys Pro Gly Leu 740 745 750 755			2314
tgc aac agc aat ggg aga tgc aca ctg gac caa aac ggc tgg cac tgc Cys Asn Ser Asn Gly Arg Cys Thr Leu Asp Gln Asn Gly Trp His Cys			2362

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760	765	770	
gtt tgc cag cca ggg tgg aga gga gca ggc tgt gac gta gcc atg gag Val Cys Gln Pro Gly Trp Arg Gly Ala Gly Cys Asp Val Ala Met Glu 775 780 785			2410
acc ctc tgt aca gac agc aaa gac aac gaa gga gac gga ctc att gac Thr Leu Cys Thr Asp Ser Lys Asp Asn Glu Gly Asp Gly Leu Ile Asp 790 795 800			2458
tgc atg gat cct gat tgc tgc ctc cag agc tcc tgc caa aac cag ccc Cys Met Asp Pro Asp Cys Cys Leu Gln Ser Ser Cys Gln Asn Gln Pro 805 810 815			2506
tac tgt cgt ggc ttg cct gat cct cag gat atc att agc caa agc ctt Tyr Cys Arg Gly Leu Pro Asp Pro Gln Asp Ile Ile Ser Gln Ser Leu 820 825 830 835			2554
cag aca cca tct cag caa gct gcc aag tcc ttc tat gac cga atc agt Gln Thr Pro Ser Gln Gln Ala Ala Lys Ser Phe Tyr Asp Arg Ile Ser 840 845 850			2602
ttc ctg att gga tgc gat agc acc cac gtg ctc cct gga gaa agt ccg Phe Leu Ile Gly Ser Asp Ser Thr His Val Leu Pro Gly Glu Ser Pro 855 860 865			2650
ttc aat aag agt ctt gcg tcc gtc atc aga ggc caa gta cta aca gct Phe Asn Lys Ser Leu Ala Ser Val Ile Arg Gly Gln Val Leu Thr Ala 870 875 880			2698
gat gga acc cca ctt att ggc gtc aac gtg tgc ttt tta cac tac tgc Asp Gly Thr Pro Leu Ile Gly Val Asn Val Ser Phe Leu His Tyr Ser 885 890 895			2746
gaa tat gga tat acc att acc cgc cag gat gga atg ttt gac ttg gtg Glu Tyr Gly Tyr Thr Ile Thr Arg Gln Asp Gly Met Phe Asp Leu Val 900 905 910 915			2794
gca aat ggt ggc gct tct ctg act ttg gta ttt gag cgt tcc cca ttc Ala Asn Gly Gly Ala Ser Leu Thr Leu Val Phe Glu Arg Ser Pro Phe 920 925 930			2842
ctc act cag tac cac act gtg tgg att ccc tgg aat gtc ttt tat gtg Leu Thr Gln Tyr His Thr Val Trp Ile Pro Trp Asn Val Phe Tyr Val 935 940 945			2890
atg gat acc ctt gtc atg aag aaa gag gag aac gac att ccc agc tgt Met Asp Thr Leu Val Met Lys Glu Glu Asn Asp Ile Pro Ser Cys 950 955 960			2938
gac ctc agt ggc ttt gtg agg cca agt ccc atc att gtg tct tca ccg Asp Leu Ser Gly Phe Val Arg Pro Ser Pro Ile Ile Val Ser Ser Pro 965 970 975			2986
tta tcc acc ttc ttc agg tct tcc cct gag gac agc ccc atc atc ccc Leu Ser Thr Phe Phe Arg Ser Ser Pro Glu Asp Ser Pro Ile Ile Pro			3034

980	985	990	995
gag aca cag gtc ctg Glu Thr Gln Val Leu 1000	cat gaa gaa acc aca His Glu Glu Thr Thr 1005	att cca gga aca gat Ile Pro Gly Thr Asp 1010	3079
ttg aaa ctt tcc tac Leu Lys Leu Ser Tyr 1015	ctg agt tcc aga gcg Leu Ser Ser Arg Ala 1020	gca ggg tac aag tca Ala Gly Tyr Lys Ser 1025	3124
gtt ctt aag att acc Val Leu Lys Ile Thr 1030	atg acc cag gcc gtc Met Thr Gln Ala Val 1035	ata ccg ttt aac ctc Ile Pro Phe Asn Leu 1040	3169
atg aag gtc cat ctg Met Lys Val His Leu 1045	atg gtg gcc gtg gtt Met Val Ala Val Val 1050	ggg aga ctc ttc cag Gly Arg Leu Phe Gln 1055	3214
aag tgg ttt cct gcc Lys Trp Phe Pro Ala 1060	tcg cca aac ttg gcc Ser Pro Asn Leu Ala 1065	tac acg ttc atc tgg Tyr Thr Phe Ile Trp 1070	3259
gat aag acg gac gca Asp Lys Thr Asp Ala 1075	tat aat cag aaa gtc Tyr Asn Gln Lys Val 1080	tac ggc ttg tca gag Tyr Gly Leu Ser Glu 1085	3304
gca gtt gtg tcc gtc Ala Val Val Ser Val 1090	gga tac gag tac gag Gly Tyr Glu Tyr Glu 1095	tcg tgc ttg gac ctg Ser Cys Leu Asp Leu 1100	3349
act ctc tgg gaa aag Thr Leu Trp Glu Lys 1105	agg act gcc gtt ttg Arg Thr Ala Val Leu 1110	caa ggc tat gag ttg Gln Gly Tyr Glu Leu 1115	3394
gat gct tcg aac atg Asp Ala Ser Asn Met 1120	ggc ggc tgg acg ttg Gly Gly Trp Thr Leu 1125	gac aag cac cat gta Asp Lys His His Val 1130	3439
ctg gac gtt cag aac Leu Asp Val Gln Asn 1135	ggt ata cta tac aaa Gly Ile Leu Tyr Lys 1140	gga aat gga gaa aat Gly Asn Gly Glu Asn 1145	3484
cag ttc atc tct cag Gln Phe Ile Ser Gln 1150	cag cct ccg gtg gtc Gln Pro Pro Val Val 1155	agc agc atc atg ggt Ser Ser Ile Met Gly 1160	3529
aat ggt cgg agg cgt Asn Gly Arg Arg Arg 1165	agc atc tca tgc cca Ser Ile Ser Cys Pro 1170	agt tgc aat ggt caa Ser Cys Asn Gly Gln 1175	3574
gct gac ggg aac aaa Ala Asp Gly Asn Lys 1180	ctc ctg gca ccc gtg Leu Leu Ala Pro Val 1185	gcg ctt gcc tgt ggg Ala Leu Ala Cys Gly 1190	3619
atc gac ggc agt cta Ile Asp Gly Ser Leu 1195	tac gta ggg gat ttc Tyr Val Gly Asp Phe 1200	aat tac gtc cgg cgg Asn Tyr Val Arg Arg 1205	3664

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1195	1200	1205	
ata ttc ccg tct ggg	aat gtg aca agt gtt	tta gaa cta aga aat	3709
Ile Phe Pro Ser Gly	Asn Val Thr Ser Val	Leu Glu Leu Arg Asn	
1210	1215	1220	
aaa gat ttt aga cat	agt agc aac cca gct	cac aga tac tac ctg	3754
Lys Asp Phe Arg His	Ser Ser Asn Pro Ala	His Arg Tyr Tyr Leu	
1225	1230	1235	
gct acg gac cca gtc	acc gga gat ttg tac	gtc tct gat act aac	3799
Ala Thr Asp Pro Val	Thr Gly Asp Leu Tyr	Val Ser Asp Thr Asn	
1240	1245	1250	
acc cgc aga atc tat	cgg ccg aaa tca ctc	acg gga gcc aaa gac	3844
Thr Arg Arg Ile Tyr	Arg Pro Lys Ser Leu	Thr Gly Ala Lys Asp	
1255	1260	1265	
ctg act aaa aac gct	gaa gtg gtg gca ggg	acc ggg gaa cag tgc	3889
Leu Thr Lys Asn Ala	Glu Val Val Ala Gly	Thr Gly Glu Gln Cys	
1270	1275	1280	
ctt ccc ttt gac gag	gcc agg tgt ggg gat	gga ggc aag gct gtg	3934
Leu Pro Phe Asp Glu	Ala Arg Cys Gly Asp	Gly Gly Lys Ala Val	
1285	1290	1295	
gaa gca acg ctc atg	agt ccc aaa gga atg	gca atc gat aag aac	3979
Glu Ala Thr Leu Met	Ser Pro Lys Gly Met	Ala Ile Asp Lys Asn	
1300	1305	1310	
gga ctg atc tac ttt	gtt gat gga acc atg	atc aga aag gtt gat	4024
Gly Leu Ile Tyr Phe	Val Asp Gly Thr Met	Ile Arg Lys Val Asp	
1315	1320	1325	
caa aat gga atc ata	tca act ctc ctg ggc	tcc aac gac ctc acg	4069
Gln Asn Gly Ile Ile	Ser Thr Leu Leu Gly	Ser Asn Asp Leu Thr	
1330	1335	1340	
tca gct cga cct tta	acc tgt gat act agc	atg cat atc agc cag	4114
Ser Ala Arg Pro Leu	Thr Cys Asp Thr Ser	Met His Ile Ser Gln	
1345	1350	1355	
gtg cgt ctg gaa tgg	ccc act gac ctc gcg	atc aac ccc atg gat	4159
Val Arg Leu Glu Trp	Pro Thr Asp Leu Ala	Ile Asn Pro Met Asp	
1360	1365	1370	
aac tcc atc tac gtc	ctg gat aat aac gta	gtt tta cag atc act	4204
Asn Ser Ile Tyr Val	Leu Asp Asn Asn Val	Val Leu Gln Ile Thr	
1375	1380	1385	
gaa aac cgt cag gtc	cgc atc gct gcc ggg	cgg ccc atg cac tgt	4249
Glu Asn Arg Gln Val	Arg Ile Ala Ala Gly	Arg Pro Met His Cys	
1390	1395	1400	
cag gtc cct gga gtg	gaa tac ccg gtg ggg	aag cac gcg gtt cag	4294
Gln Val Pro Gly Val	Glu Tyr Pro Val Gly	Lys His Ala Val Gln	

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1405					1410					1415					
acc acc ctg gag tca	gcc acg gcc att gct	gtg tcc tac agc ggg	4339												
Thr Thr Leu Glu Ser	Ala Thr Ala Ile Ala	Val Ser Tyr Ser Gly													
1420		1425		1430											
gtc ctt tac atc acg	gaa act gat gag aag	aag atc aac cga ata	4384												
Val Leu Tyr Ile Thr	Glu Thr Asp Glu Lys	Lys Ile Asn Arg Ile													
1435		1440		1445											
agg cag gtc acg aca	gac ggg gag atc tcc	tta gtg gct ggg ata	4429												
Arg Gln Val Thr Thr	Asp Gly Glu Ile Ser	Leu Val Ala Gly Ile													
1450		1455		1460											
cct tcg gaa tgt gac	tgc aag aac gac gcc	aac tgt gac tgc tac	4474												
Pro Ser Glu Cys Asp	Cys Lys Asn Asp Ala	Asn Cys Asp Cys Tyr													
1465		1470		1475											
caa agc gga gac ggc	tac gcc aaa gat gcc	aaa ctc aat gcg ccg	4519												
Gln Ser Gly Asp Gly	Tyr Ala Lys Asp Ala	Lys Leu Asn Ala Pro													
1480		1485		1490											
tcc tcc ctg gcc gcc	tcg cca gat ggc act	ctg tac att gca gat	4564												
Ser Ser Leu Ala Ala	Ser Pro Asp Gly Thr	Leu Tyr Ile Ala Asp													
1495		1500		1505											
ctg gga aat atc agg	atc cgg gcc gtt tcg	aag aat aaa cct tta	4609												
Leu Gly Asn Ile Arg	Ile Arg Ala Val Ser	Lys Asn Lys Pro Leu													
1510		1515		1520											
ctg aac tca atg aac	ttt tac gaa gtt gcc	tct cca act gat caa	4654												
Leu Asn Ser Met Asn	Phe Tyr Glu Val Ala	Ser Pro Thr Asp Gln													
1525		1530		1535											
gag ctc tac atc ttt	gac atc aac ggt act	cac cag tac acc gtg	4699												
Glu Leu Tyr Ile Phe	Asp Ile Asn Gly Thr	His Gln Tyr Thr Val													
1540		1545		1550											
agc ctg gtc acg ggt	gac tac cta tat aat	ttt agt tac agc aat	4744												
Ser Leu Val Thr Gly	Asp Tyr Leu Tyr Asn	Phe Ser Tyr Ser Asn													
1555		1560		1565											
gac aat gac gtc acc	gct gta act gac agc	aat ggc aac acc ctc	4789												
Asp Asn Asp Val Thr	Ala Val Thr Asp Ser	Asn Gly Asn Thr Leu													
1570		1575		1580											
cga atc cga agg gat	ccg aat cgg atg ccg	gtg cgg gtg gtg tct	4834												
Arg Ile Arg Arg Asp	Pro Asn Arg Met Pro	Val Arg Val Val Ser													
1585		1590		1595											
cct gat aac cag gtg	ata tgg ttg acc ata	ggc acc aac ggg tgt	4879												
Pro Asp Asn Gln Val	Ile Trp Leu Thr Ile	Gly Thr Asn Gly Cys													
1600		1605		1610											
ctg aaa agc atg acc	gct cag ggc ctg gaa	ctg gtt ttg ttt act	4924												
Leu Lys Ser Met Thr	Ala Gln Gly Leu Glu	Leu Val Leu Phe Thr													



	1615		1620		1625	
tac cat ggc aac agt	ggg ctt tta gcc acc	aaa agt gac gaa act	4969			
Tyr His Gly Asn Ser	Gly Leu Leu Ala Thr	Lys Ser Asp Glu Thr				
	1630	1635		1640		
gga tgg aca aca ttt	ttt gac tat gac agt	gaa ggt cgc ctg acg	5014			
Gly Trp Thr Thr Phe	Phe Asp Tyr Asp Ser	Glu Gly Arg Leu Thr				
	1645	1650		1655		
aat gtt acc ttc ccc	act ggg gtg gtt aca	aac ctg cac ggg gac	5059			
Asn Val Thr Phe Pro	Thr Gly Val Val Thr	Asn Leu His Gly Asp				
	1660	1665		1670		
atg gac aag gct atc	acg gtg gac atc gag	tca tcc agc aga gag	5104			
Met Asp Lys Ala Ile	Thr Val Asp Ile Glu	Ser Ser Ser Arg Glu				
	1675	1680		1685		
gaa gat gtc agc atc	act tcg aac ttg tcc	tcc atc gat tcc ttc	5149			
Glu Asp Val Ser Ile	Thr Ser Asn Leu Ser	Ser Ile Asp Ser Phe				
	1690	1695		1700		
tac acc atg gtc caa	gac cag tta aga aac	agt tac cag att ggg	5194			
Tyr Thr Met Val Gln	Asp Gln Leu Arg Asn	Ser Tyr Gln Ile Gly				
	1705	1710		1715		
tat gat ggc tcc ctt	aga atc ttc tat gcc	agt ggt ctg gac tct	5239			
Tyr Asp Gly Ser Leu	Arg Ile Phe Tyr Ala	Ser Gly Leu Asp Ser				
	1720	1725		1730		
cac tac cag aca gag	ccc cac gtt ctg gct	ggc acg gcg aat ccc	5284			
His Tyr Gln Thr Glu	Pro His Val Leu Ala	Gly Thr Ala Asn Pro				
	1735	1740		1745		
aca gta gcc aaa aga	aac atg act ctt ccc	ggc gag aac ggg cag	5329			
Thr Val Ala Lys Arg	Asn Met Thr Leu Pro	Gly Glu Asn Gly Gln				
	1750	1755		1760		
aat ctg gtg gag tgg	aga ttc cga aaa gaa	caa gcc cag ggc aaa	5374			
Asn Leu Val Glu Trp	Arg Phe Arg Lys Glu	Gln Ala Gln Gly Lys				
	1765	1770		1775		
gtc aac gta ttc ggc	cgg aag ctc agg gtc	aat ggg cgc aac cta	5419			
Val Asn Val Phe Gly	Arg Lys Leu Arg Val	Asn Gly Arg Asn Leu				
	1780	1785		1790		
ctc tca gtg gac ttt	gat cgg acc acc aag	acg gaa aag atc tat	5464			
Leu Ser Val Asp Phe	Asp Arg Thr Thr Lys	Thr Glu Lys Ile Tyr				
	1795	1800		1805		
gat gac cac cgg aaa	ttt ctc ctg agg atc	gct tac gac acg tcg	5509			
Asp Asp His Arg Lys	Phe Leu Leu Arg Ile	Ala Tyr Asp Thr Ser				
	1810	1815		1820		
ggg cac ccg act ctc	tgg ctg ccg agt agc	aag cta atg gca gtg	5554			
Gly His Pro Thr Leu	Trp Leu Pro Ser Ser	Lys Leu Met Ala Val				

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1825	1830	1835	
aac gtc acc tac tca	tcc acc ggt caa att	gcc agc atc cag aga	5599
Asn Val Thr Tyr Ser	Ser Thr Gly Gln Ile	Ala Ser Ile Gln Arg	
1840	1845	1850	
ggg acc acg agc gaa	aag gtg gac tat gac	agc cag ggg agg atc	5644
Gly Thr Thr Ser Glu	Lys Val Asp Tyr Asp	Ser Gln Gly Arg Ile	
1855	1860	1865	
gta tct cgg gtc ttt	gcc gat ggg aaa aca	tgg agt tac acg tac	5689
Val Ser Arg Val Phe	Ala Asp Gly Lys Thr	Trp Ser Tyr Thr Tyr	
1870	1875	1880	
ttg gaa aag tcc atg	gtt ctt ctg ctc cat	agc cag cgg cag tac	5734
Leu Glu Lys Ser Met	Val Leu Leu Leu His	Ser Gln Arg Gln Tyr	
1885	1890	1895	
atc ttc gaa tac gac	atg tgg gac cgc ctg	tcc gcc atc acc atg	5779
Ile Phe Glu Tyr Asp	Met Trp Asp Arg Leu	Ser Ala Ile Thr Met	
1900	1905	1910	
ccc agt gtg gct cgc	cac acc atg cag acc	atc cgg tcc att ggc	5824
Pro Ser Val Ala Arg	His Thr Met Gln Thr	Ile Arg Ser Ile Gly	
1915	1920	1925	
tac tac cgc aac atc	tac aat ccc cca gaa	agc aat gcc tct atc	5869
Tyr Tyr Arg Asn Ile	Tyr Asn Pro Pro Glu	Ser Asn Ala Ser Ile	
1930	1935	1940	
atc acc gac tac aac	gag gaa ggg ctg ctt	ctg caa aca gct ttc	5914
Ile Thr Asp Tyr Asn	Glu Glu Gly Leu Leu	Leu Gln Thr Ala Phe	
1945	1950	1955	
ctg gga acg agt cgg	agg gtc tta ttc aag	tat aga agg cag acc	5959
Leu Gly Thr Ser Arg	Arg Val Leu Phe Lys	Tyr Arg Arg Gln Thr	
1960	1965	1970	
agg cta tca gaa att	tta tac gac agc aca	aga gtc agt ttt acc	6004
Arg Leu Ser Glu Ile	Leu Tyr Asp Ser Thr	Arg Val Ser Phe Thr	
1975	1980	1985	
tac gac gaa aca gcg	gga gtc ctg aaa aca	gta aac ctt cag agt	6049
Tyr Asp Glu Thr Ala	Gly Val Leu Lys Thr	Val Asn Leu Gln Ser	
1990	1995	2000	
gat ggt ttt att tgc	acc att aga tac agg	caa att ggt ccc ctg	6094
Asp Gly Phe Ile Cys	Thr Ile Arg Tyr Arg	Gln Ile Gly Pro Leu	
2005	2010	2015	
att gac aga cag att	ttc cgc ttc agc gag	gat gga atg gta aat	6139
Ile Asp Arg Gln Ile	Phe Arg Phe Ser Glu	Asp Gly Met Val Asn	
2020	2025	2030	
gcg aga ttt gac tat	agc tac gac aac agc	ttt cga gtg acc agc	6184
Ala Arg Phe Asp Tyr	Ser Tyr Asp Asn Ser	Phe Arg Val Thr Ser	

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2035	2040	2045	
atg cag ggt gtc atc	aat gaa aca cca ctg	ccc att gat cta tac	6229
Met Gln Gly Val Ile	Asn Glu Thr Pro Leu	Pro Ile Asp Leu Tyr	
2050	2055	2060	
cag ttt gat gac atc	tct ggc aaa gtc gag	cag ttt gga aaa ttc	6274
Gln Phe Asp Asp Ile	Ser Gly Lys Val Glu	Gln Phe Gly Lys Phe	
2065	2070	2075	
gga gtg ata tac tac	gac atc aac caa atc	att tcc acg gcc gtg	6319
Gly Val Ile Tyr Tyr	Asp Ile Asn Gln Ile	Ile Ser Thr Ala Val	
2080	2085	2090	
atg act tat aca aag	cac ttt gat gct cat	ggg cgc atc aag gag	6364
Met Thr Tyr Thr Lys	His Phe Asp Ala His	Gly Arg Ile Lys Glu	
2095	2100	2105	
atc caa tat gag ata	ttt agg tca ctc atg	tac tgg att aca att	6409
Ile Gln Tyr Glu Ile	Phe Arg Ser Leu Met	Tyr Trp Ile Thr Ile	
2110	2115	2120	
caa tat gat aat atg	ggc cgg gta acc aag	aga gag att aaa att	6454
Gln Tyr Asp Asn Met	Gly Arg Val Thr Lys	Arg Glu Ile Lys Ile	
2125	2130	2135	
ggg cct ttt gcc aac	act acc aaa tac gcg	tac gag tac gac gtc	6499
Gly Pro Phe Ala Asn	Thr Thr Lys Tyr Ala	Tyr Glu Tyr Asp Val	
2140	2145	2150	
gat gga cag ctc caa	aca gtt tac cta aac	gaa aag atc atg tgg	6544
Asp Gly Gln Leu Gln	Thr Val Tyr Leu Asn	Glu Lys Ile Met Trp	
2155	2160	2165	
cgg tac aac tac gac	cta aat gga aac ctc	cac ttg ctc aac ccc	6589
Arg Tyr Asn Tyr Asp	Leu Asn Gly Asn Leu	His Leu Leu Asn Pro	
2170	2175	2180	
agc agc agc gcc cgc	ctg acc cct ctg cgc	tat gac ctg cgc gac	6634
Ser Ser Ser Ala Arg	Leu Thr Pro Leu Arg	Tyr Asp Leu Arg Asp	
2185	2190	2195	
aga atc acc cgc ctg	ggc gat gtt cag tac	cgg ctg gat gaa gat	6679
Arg Ile Thr Arg Leu	Gly Asp Val Gln Tyr	Arg Leu Asp Glu Asp	
2200	2205	2210	
ggt ttc ctg cgt cag	agg ggc act gaa att	ttt gaa tac agc tcc	6724
Gly Phe Leu Arg Gln	Arg Gly Thr Glu Ile	Phe Glu Tyr Ser Ser	
2215	2220	2225	
aaa ggg ctt ctg act	cga gtc tac agt aaa	ggc agt ggc tgg aca	6769
Lys Gly Leu Leu Thr	Arg Val Tyr Ser Lys	Gly Ser Gly Trp Thr	
2230	2235	2240	
gtg atc tat cgg tac	gac ggc ctg gga aga	cgt gtt tct agc aaa	6814
Val Ile Tyr Arg Tyr	Asp Gly Leu Gly Arg	Arg Val Ser Ser Lys	

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2245	2250	2255	
acc agc ctg gga cag	cac ctt cag ttt ttc	tac gcc gac ctg aca	6859
Thr Ser Leu Gly Gln	His Leu Gln Phe Phe	Tyr Ala Asp Leu Thr	
2260	2265	2270	
tac ccc acg aga att	act cac gtc tac aac	cat tcc agt tca gaa	6904
Tyr Pro Thr Arg Ile	Thr His Val Tyr Asn	His Ser Ser Ser Glu	
2275	2280	2285	
atc acc tcc ctg tac	tat gac ctc caa gga	cat ctc ttc gcc atg	6949
Ile Thr Ser Leu Tyr	Tyr Asp Leu Gln Gly	His Leu Phe Ala Met	
2290	2295	2300	
gag atc agc agt ggg	gat gag ttc tac atc	gcc tcg gac aac acg	6994
Glu Ile Ser Ser Gly	Asp Glu Phe Tyr Ile	Ala Ser Asp Asn Thr	
2305	2310	2315	
ggg aca ccg ctg gct	gtt ttc agc agc aac	ggg ctc atg ctg aaa	7039
Gly Thr Pro Leu Ala	Val Phe Ser Ser Asn	Gly Leu Met Leu Lys	
2320	2325	2330	
cag acc cag tac act	gcc tat ggt gag atc	tac ttt gac tcc aac	7084
Gln Thr Gln Tyr Thr	Ala Tyr Gly Glu Ile	Tyr Phe Asp Ser Asn	
2335	2340	2345	
gtc gac ttt cag ctg	gta att gga ttc cac	ggg ggc ttg tat gac	7129
Val Asp Phe Gln Leu	Val Ile Gly Phe His	Gly Gly Leu Tyr Asp	
2350	2355	2360	
ccg ctc acc aaa cta	atc cac ttt gga gaa	aga gat tat gac att	7174
Pro Leu Thr Lys Leu	Ile His Phe Gly Glu	Arg Asp Tyr Asp Ile	
2365	2370	2375	
ttg gcg gga aga tgg	acc aca ccg gac att	gaa atc tgg aaa agg	7219
Leu Ala Gly Arg Trp	Thr Thr Pro Asp Ile	Glu Ile Trp Lys Arg	
2380	2385	2390	
atc gga aag gac cct	gct cct ttt aac ctg	tat atg ttt cgg aat	7264
Ile Gly Lys Asp Pro	Ala Pro Phe Asn Leu	Tyr Met Phe Arg Asn	
2395	2400	2405	
aac aac ccc gcg agc	aaa atc cat gat gtg	aaa gat tac atc acg	7309
Asn Asn Pro Ala Ser	Lys Ile His Asp Val	Lys Asp Tyr Ile Thr	
2410	2415	2420	
gat gtt aac agc tgg	ctg gtg acg ttt ggc	ttc cat ctg cac aat	7354
Asp Val Asn Ser Trp	Leu Val Thr Phe Gly	Phe His Leu His Asn	
2425	2430	2435	
gct att cct gga ttc	cct gtt ccc aaa ttt	gat tta act gag cct	7399
Ala Ile Pro Gly Phe	Pro Val Pro Lys Phe	Asp Leu Thr Glu Pro	
2440	2445	2450	
tcc tat gag ctt gtg	aag agt caa cag tgg	gaa gat gtg ccg ccc	7444
Ser Tyr Glu Leu Val	Lys Ser Gln Gln Trp	Glu Asp Val Pro Pro	

2455	2460	2465	
atc ttt gga gtt cag	cag caa gtg gca agg	caa gcc aag gcc ttc	7489
Ile Phe Gly Val Gln	Gln Gln Val Ala Arg	Gln Ala Lys Ala Phe	
2470	2475	2480	
ttg tcc ctg ggg aag	atg gcc gag gtg cag	gtg agc cga cgc aaa	7534
Leu Ser Leu Gly Lys	Met Ala Glu Val Gln	Val Ser Arg Arg Lys	
2485	2490	2495	
gct ggc gcc gag cag	tcg tgg ctg tgg ttc	gcc acg gtc aag tcg	7579
Ala Gly Ala Glu Gln	Ser Trp Leu Trp Phe	Ala Thr Val Lys Ser	
2500	2505	2510	
ctc atc ggc aag ggc	gtc atg ctg gcc gtg	agc caa ggc cgc gtg	7624
Leu Ile Gly Lys Gly	Val Met Leu Ala Val	Ser Gln Gly Arg Val	
2515	2520	2525	
cag acc aac gtg ctc	aac atc gcc aac gag	gac tgc atc aag gtg	7669
Gln Thr Asn Val Leu	Asn Ile Ala Asn Glu	Asp Cys Ile Lys Val	
2530	2535	2540	
gcg gcg gtg ctc aac	aac gcc ttc tac ctg	gag aac ctg cac ttc	7714
Ala Ala Val Leu Asn	Asn Ala Phe Tyr Leu	Glu Asn Leu His Phe	
2545	2550	2555	
acc atc gag ggc aag	gac aca cac tac ttc	atc aag acc acc aca	7759
Thr Ile Glu Gly Lys	Asp Thr His Tyr Phe	Ile Lys Thr Thr Thr	
2560	2565	2570	
ccc gag agc gac ctg	ggc aca ctg cgg ctg	acg agc ggt cgc aag	7804
Pro Glu Ser Asp Leu	Gly Thr Leu Arg Leu	Thr Ser Gly Arg Lys	
2575	2580	2585	
gcc ctg gag aac ggg	atc aac gtg acc gtg	tct cag tcc acc acg	7849
Ala Leu Glu Asn Gly	Ile Asn Val Thr Val	Ser Gln Ser Thr Thr	
2590	2595	2600	
gtg gtg aac ggc agg	act cgc agg ttc gcc	gac gtg gag atg cag	7894
Val Val Asn Gly Arg	Thr Arg Arg Phe Ala	Asp Val Glu Met Gln	
2605	2610	2615	
ttc ggt gcc ctg gca	ctg cat gtg cgc tat	ggc atg acg ctg gac	7939
Phe Gly Ala Leu Ala	Leu His Val Arg Tyr	Gly Met Thr Leu Asp	
2620	2625	2630	
gag gag aag gcg cgc	att ctg gag cag gcg	cgc cag cgc gcg ctc	7984
Glu Glu Lys Ala Arg	Ile Leu Glu Gln Ala	Arg Gln Arg Ala Leu	
2635	2640	2645	
gcc cgg gcg tgg gca	cgg gag cag cag cgc	gtg cgc gac ggc gag	8029
Ala Arg Ala Trp Ala	Arg Glu Gln Gln Arg	Val Arg Asp Gly Glu	
2650	2655	2660	
gag ggt gcg cgc ctc	tgg acg gag ggt gag	aaa cgg cag ctg ctg	8074
Glu Gly Ala Arg Leu	Trp Thr Glu Gly Glu	Lys Arg Gln Leu Leu	

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2665	2670	2675	
agc gct ggc aag gtg	cag ggc tac gat ggg	tac tac gta ctg tcg	8119
Ser Ala Gly Lys Val	Gln Gly Tyr Asp Gly	Tyr Tyr Val Leu Ser	
2680	2685	2690	
gtg gag cag tac ccc	gag ctg gct gac agt	gcc aac aac atc cag	8164
Val Glu Gln Tyr Pro	Glu Leu Ala Asp Ser	Ala Asn Asn Ile Gln	
2695	2700	2705	
ttc ttg cga caa agt	gag atc ggc aag agg	taa cccccgggcc	8207
Phe Leu Arg Gln Ser	Glu Ile Gly Lys Arg		
2710	2715		
accctgtgc agattctcct gtagcacaat ccaaaccgga ctctccaaag agccttccaa			8267
aatgacactg ctctgcagac agacacatcg cagatacaca cgcaacacaa accagaaaca			8327
aagacaactt tttttttttt ctgaatgacc ttaaagggtga tcggctttta agaatatgtt			8387
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			Met Tyr Ser

gtt gac cgt gtg tct gac gac atc cct att cgt acc tgg ttc ccc aag	163
Val Asp Arg Val Ser Asp Asp Ile Pro Ile Arg Thr Trp Phe Pro Lys	
5 10 15	
gaa aat ctt ttc agc ttc cag aca gca acc aca act atg caa gcg gtg	211
Glu Asn Leu Phe Ser Phe Gln Thr Ala Thr Thr Thr Met Gln Ala Val	
20 25 30 35	
ttc agg ggc tac gcg gag agg aag cgc cgg aaa cgg gag aat gat tcc	259
Phe Arg Gly Tyr Ala Glu Arg Lys Arg Arg Lys Arg Glu Asn Asp Ser	
40 45 50	
gcg tct gta atc cag agg aac ttc cgc aaa cac ctg cgc atg gtc ggc	307
Ala Ser Val Ile Gln Arg Asn Phe Arg Lys His Leu Arg Met Val Gly	
55 60 65	
agc cgg agg gtg aag gcc cag acg ttc gct gag cgg cgc gag cgg agc	355
Ser Arg Arg Val Lys Ala Gln Thr Phe Ala Glu Arg Arg Glu Arg Ser	
70 75 80	
ttc agc cgg tcc tgg agc gac ccc acc ccc atg aaa gcc gac act tcc	403
Phe Ser Arg Ser Trp Ser Asp Pro Thr Pro Met Lys Ala Asp Thr Ser	
85 90 95	
cac gac tcc cga gac agc agt gac ctg cag agc tcc cac tgc acg ctg	451
His Asp Ser Arg Asp Ser Ser Asp Leu Gln Ser Ser His Cys Thr Leu	
100 105 110 115	
gac gag gcc ttc gag gac ctg gac tgg gac act gag aag ggc ctg gag	499
Asp Glu Ala Phe Glu Asp Leu Asp Trp Asp Thr Glu Lys Gly Leu Glu	
120 125 130	
gct gtg gcc tgc gac acc gaa ggc ttc gtg cca cca aag gtc atg ctc	547
Ala Val Ala Cys Asp Thr Glu Gly Phe Val Pro Pro Lys Val Met Leu	
135 140 145	
att tcc tcc aag gtg ccc aag gct gag tac atc ccc act atc atc cgc	595
Ile Ser Ser Lys Val Pro Lys Ala Glu Tyr Ile Pro Thr Ile Ile Arg	
150 155 160	
cgg gat gac ccc tcc atc atc ccc atc ctc tac gac cat gag cac gca	643
Arg Asp Asp Pro Ser Ile Ile Pro Ile Leu Tyr Asp His Glu His Ala	
165 170 175	
acc ttc gag gac atc ctt gag gag ata gag agg aag ctg aac gtc tac	691
Thr Phe Glu Asp Ile Leu Glu Glu Ile Glu Arg Lys Leu Asn Val Tyr	
180 185 190 195	
cac aag gga gcc aag atc tgg aaa atg ctg att ttc tgc cag gga ggt	739
His Lys Gly Ala Lys Ile Trp Lys Met Leu Ile Phe Cys Gln Gly Gly	
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cct gga cac ctc tat ctc ctc aag aac aag gtg gcc acc ttt gcc aaa	787
Pro Gly His Leu Tyr Leu Leu Lys Asn Lys Val Ala Thr Phe Ala Lys	

215	220	225	
gtg gag aag gaa gag gac atg att cac ttc tgg aag cgg ctg agc cgc			835
Val Glu Lys Glu Glu Asp Met Ile His Phe Trp Lys Arg Leu Ser Arg			
230	235	240	
ctg atg agc aaa gtg aac cca gag cgg aac gtc atc cac atc atg ggc			883
Leu Met Ser Lys Val Asn Pro Glu Pro Asn Val Ile His Ile Met Gly			
245	250	255	
tgc tac att ctg ggg aac ccc aat gga gag aag ctg ttc cag aac ctc			931
Cys Tyr Ile Leu Gly Asn Pro Asn Gly Glu Lys Leu Phe Gln Asn Leu			
260	265	270	275
agg acc ctc atg act cct tat agg gtc acc ttc gag tca ccc ctg gag			979
Arg Thr Leu Met Thr Pro Tyr Arg Val Thr Phe Glu Ser Pro Leu Glu			
280	285	290	
ctc tca gcc caa ggg aag cag atg atc gag acg tac ttt gac ttc cgg			1027
Leu Ser Ala Gln Gly Lys Gln Met Ile Glu Thr Tyr Phe Asp Phe Arg			
295	300	305	
ttg tat cgc ctg tgg aag agc cgc cag cac tcg aag ctg ctg gac ttt			1075
Leu Tyr Arg Leu Trp Lys Ser Arg Gln His Ser Lys Leu Leu Asp Phe			
310	315	320	
gac gac gtc ctg tga ggggcagagg cctccgccca gtcaccatca ggccactccc			1130
Asp Asp Val Leu			
325			
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Trp Ala Gly Pro Ala Thr Ser Ala Asp Leu Arg Ser Pro Gln Glu  
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gct gga gag gat gta cag cgt tga ccg tgt gtc tga cga cat ccc tat 144  
Ala Gly Glu Asp Val Gln Arg Pro Cys Val Arg His Pro Tyr  
35 40 45  
tcg tac ctg gtt ccc caa gga aaa tct ttt cag ctt cca gac agc aac 192  
Ser Tyr Leu Val Pro Gln Gly Lys Ser Phe Gln Leu Pro Asp Ser Asn  
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cac aac tat gca agc ggt gtt cag ggg cta cgc gga gag gaa gcg ccg 240  
His Asn Tyr Ala Ser Gly Val Gln Gly Leu Arg Gly Glu Glu Ala Pro  
65 70 75  
gaa acg gga gaa tga ttc cgc gtc tgt aat cca gag gaa ctt ccg caa 288  
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<223> TCAP 3 General Motif

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<222> (6)..(6)

<223> X=G or R

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<223> X=V or I

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Leu Ser Xaa Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Xaa  
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Gln Phe Leu Arg Gln Ser Glu Ile  
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&lt;223&gt; G. gallus TCAP2

&lt;400&gt; 136

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Gln Asn Glu Met  
 35

&lt;210&gt; 137

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human Ten M1

&lt;400&gt; 137

Thr Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe  
 1 5 10 15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Arg Tyr Asn Asp Gly Arg  
 20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val  
 35 40 45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala  
 50 55 60

Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile Leu  
 65 70 75 80

Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Arg  
 85 90 95

Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu Val  
 100 105 110

77/77

Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val Asn  
115 120 125

Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg Arg  
130 135 140

Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile Arg  
145 150 155 160

Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Ile Ala  
165 170 175

Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Lys Glu Gln Arg Arg Leu  
180 185 190

Gln Glu Gly Glu Glu Gly Ile Arg Ala Trp Thr Glu Gly Glu Lys Gln  
195 200 205

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val  
210 215 220

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile  
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His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
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<212> PRT

<213> Artificial Sequence

<220>

<223> G. gallus TCAP-1

<400> 138

Gln Leu Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile  
20 25 30

His Phe Met Arg Gln Ser Glu Ile  
35 40